



SEQUENCE LISTING

<110> DIVERSA CORPORATION
SHORT, Jay
KRETZ, Keith

<120> RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

<130> DIVER1370-6

<140> US 09/777,566

<141> 2001-02-05

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

<151> 1999-04-13

<150> US 09/259,214

<151> 1999-03-01

<150> US 08/910,798

<151> 1997-08-13

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 1323

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1320)

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<221> misc_feature

<222> (1)..(1323)

<223> n is any nucleotide

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ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
20 25 30

gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
35 40 45

caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
50 55 60

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144

192

aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc	240
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa	288
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	
85 90 95	
aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac	336
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct	384
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat	432
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
130 135 140	
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg	480
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
145 150 155 160	
aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac	528
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp	
165 170 175	
ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt	576
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
180 185 190	
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa	624
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu	
195 200 205	
agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc	672
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala	
210 215 220	
gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg	720
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr	
225 230 235 240	
gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg	768
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp	
245 250 255	
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat	816
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His	
260 265 270	
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc	864
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser	
275 280 285	
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat	912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His	
290 295 300	
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg	960

Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320

 ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg 1008
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335

 gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt 1056
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350

 ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag 1104
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365

 tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat 1152
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380

 aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc 1200
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400

 ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca 1248
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 405 410 415

 ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg 1296
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430

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 Arg Ser His His His His His His
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 <213> Escherichia coli

 <220>
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 <222> (1)..(1323)
 <223> n is any nucleotide

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 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
 1 5 10 15

 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
 20 25 30

 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 35 40 45

 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val

50	55	60
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu 65 70 75 80		
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys 85 90 95		
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp 100 105 110		
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro 115 120 125		
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp 130 135 140		
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala 145 150 155 160		
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp 165 170 175		
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu 180 185 190		
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu 195 200 205		
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala 210 215 220		
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr 225 230 235 240		
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp 245 250 255		
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His 260 265 270		
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser 275 280 285		
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His 290 295 300		

Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
305 310 315 320

Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
325 330 335

Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
340 345 350

Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
355 360 365

Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
370 375 380

Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
385 390 395 400

Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
405 410 415

Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
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Arg Ser His His His His His His
435 440

<210> 3
<211> 49
<212> DNA
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<223> Primer for PCR

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gtttctgaat tcaaggagga atttaaataa aagcgatctt aatcccatt

49

<210> 4
<211> 33
<212> DNA
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<220>
<223> Primer for PCR

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